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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: December 13, 2002, 22:53:08 ; Search time 44 Seconds

Title: US-09-659-737A-2

Perfect score: 293

Sequence: 1 HRDIKAGNILLKEIHD... EWHTTTRMSTAGTYAWMAPE 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR:73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	239	81.6	394	JU0229 mixed-lineage protein kinase 1 - human
2	231	78.8	847	1 A53800 C;Species: Homo sapiens (man)
3	216	73.7	954	1 S68178 C;Accession: S32467; JU0229
4	127	43.3	436	2 T48205 R;DOROW, D.S.; BEVEREUX, L.; DIETTSCH, E.; DE KRETSER, T.
5	124.5	42.5	668	2 JC2363 Bur. J. Biochem. 213/ 701-710, 1973
6	124.5	42.5	888	2 A55318 A;Title: Identification of a new family of human epithelial protein kinases containing
7	124.5	42.5	356	2 T48205 A;Reference number: S32467; PMID:847742
8	121.5	41.5	111	2 I38218 A;Molecule type: mRNA
9	121	41.3	356	2 S61766 A;Residues: 1-394 <DQ2>
10	114.5	39.1	545	2 T05675 C;Genet. test:
11	111	37.9	406	2 T52626 A;Gene: GDB:MIKL1
12	111	37.9	885	2 T48544 A;Cross-references: GDB:141921; OMIM:600136
13	111	37.9	1030	2 F96763 A;CDS position: 14924-3-4931
14	107.5	36.7	1478	2 S20117 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologous domain
15	107.5	36.7	407	2 G84635 C;Keywords: RIP; leucine zipper; phosphotransferase; serine/threonine-specific protein kinase
16	107.5	36.7	1338	2 T30565 R;1-269/Domain: protein kinase homology <KIN>
17	107	36.5	816	2 T45684 R;2-268/Region: catalytic <CAT>
18	107	36.5	836	2 B96716 R;3-268/Region: protein kinase ATP-binding motif
19	106.5	36.3	377	2 T46149 R;4-268/Region: leucine zipper motif
20	106	36.2	731	2 T04455 R;5-268/Region: basic
21	106	36.2	847	2 T14375 R;6-268/Region: basic
22	106	36.2	1015	2 T00726 R;7-268/Region: basic
23	105.5	36.0	649	2 B96729 R;8-268/Region: basic
24	105	35.8	844	1 T05179 R;9-268/Region: basic
25	104.5	35.7	381	2 H96731 R;10-268/Region: basic
26	104.5	35.7	412	2 T10671 R;11-268/Region: basic
27	104.5	35.7	1021	2 A86424 R;12-268/Region: basic
28	104	35.5	581	2 T04552 R;13-268/Region: basic
29	104	35.5	690	2 C96572 R;14-268/Region: basic

RESULT 1

JU0229 mixed-lineage protein kinase 1 - human

C;Species: Homo sapiens (man)

C;Accession: S32467; JU0229

R;DOROW, D.S.; BEVEREUX, L.; DIETTSCH, E.; DE KRETSER, T.

Bur. J. Biochem. 213/ 701-710, 1973

A;Title: Identification of a new family of human epithelial protein kinases containing

A;Reference number: S32467; PMID:93238756; PMID:847742

A;Molecule type: mRNA

A;Residues: 1-394 <DQ2>

A;Gene: GDB:MIKL1

A;Cross-references: GDB:141921; OMIM:600136

A;CDS position: 14924-3-4931

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologous domain

C;Keywords: RIP; leucine zipper; phosphotransferase; serine/threonine-specific protein kinase

R;1-269/Domain: protein kinase homology <KIN>

R;2-268/Region: catalytic <CAT>

R;3-268/Region: protein kinase ATP-binding motif

R;4-268/Region: leucine zipper motif

R;5-268/Region: basic

R;6-268/Region: basic

R;7-268/Region: basic

R;8-268/Region: basic

R;9-268/Region: basic

R;10-268/Region: basic

R;11-268/Region: basic

R;12-268/Region: basic

R;13-268/Region: basic

R;14-268/Region: basic

R;15-268/Region: basic

R;16-268/Region: basic

R;17-268/Region: basic

R;18-268/Region: basic

R;19-268/Region: basic

R;20-268/Region: basic

R;21-268/Region: basic

R;22-268/Region: basic

R;23-268/Region: basic

R;24-268/Region: basic

R;25-268/Region: basic

R;26-268/Region: basic

R;27-268/Region: basic

R;28-268/Region: basic

R;29-268/Region: basic

RESULT 2

A;Accession: A53800

N;Alternate names: protein kinase PK1; protein kinase SPRK

C;Species: Homo sapiens (man)

C;Accession: A53800; 158395

R;Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, O.; Godowski, P.J.

J. Biol. Chem. 269, 1502-1510, 1994

A;Title: Identification and characterization of SPRK, a novel src-homology 3 domain-containing protein kinase

A;Reference number: A53800; PMID:9425068; PMID:8195146

A;Accession: A53800

A;Status: preliminary

A;Residues: 1-847 <GA>

A;Molecule type: mRNA

A;Cross-references: GDB:00747; PID:AAA19647; PID:9464028

R;Inq, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.

Oncogene 9, 1745-1750, 1994

A;Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain

A;Reference number: 188395; MUID:94239754; PMID:818572

A;Accession: 158395; Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-847 <RIN>

A;Cross-references: GB:132976; NID:9488295; PIDN:AAA59859.1; PID:9488296

A;Genetics: C;Genetics:

A;Gene: GDB:MLK3; PTKL; SPRK

A;Cross-references: GDB:134755; OMIM:600050

C;Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology; serine/threonine-specific protein kinase

C;Keywords: Atp; leucine zipper; phosphotransferase; serine/threonine-specific protein kinase

F;48-100/Domain: SH3 homology <SH3>

F;111-383/Domain: protein kinase homology <KIN>

F;121-311/Region: protein kinase Atp-binding motif

F;40-424/Region: leucine zipper motif

F;438-459/Region: leucine zipper motif

F;468-482/Region: basic

RESULT 3

Query Match Best Local Similarity 78.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

RESULT 3

Query Match Best Local Similarity 77.8%; Score 231; DB 1; Length 847; Matches 42; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 239 HRDIKSNNNILLQPIESDDMMHKTLKITDGLAREWHRTTOMSAQTYAWAPE 292

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

RESULT 4

Query Match Best Local Similarity 73.7%; Score 216; DB 1; Length 954; Matches 39; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Oy 1 HRDIKAGNITLLEKIEHDIDCNKTKITPGLAREWHRRTKYSTAGTYAWAPE 54

Db 220 HRDLKSINILILEAENHNLADEVTKIKIDFGLAREWHRKTMSAGTYAWAPE 273

Best Local Similarity 50.9%; Pred. No. 5.2e-05; Indels 9; Gaps 3; Matches 28; Conservative 11; Mismatches 9;

RESULT 6
 Query 1 HRDIKAGNINILLEKEHDDICNKTLKITDFGLAREW-HRTIKSTACTYAWAPE 54
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Sep-1999
 C;Accession: A55318
 R;Holzman, L.B.; Merritt, S.E.; Fan, G.
 J. Biol. Chem. 269, 30808-30817, 1994
 A;Title: Identification, molecular cloning, and characterization of dual leucine zipper proteins. Identification of 21 novel human protein kinases, including 3 members of a family.
 A;Reference number: A55318; MUID:95074107; PMID:7983011
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-808
 A;Cross-references: GB:U14636; NID:9602677; PIDN:CAA5280 1; PID:5602678
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs; protein kinase homology <KIN>
 C;Keywords: ATP; leucine zipper; phosphotransferase F;156-104/Region: protein kinase ATP-binding motif F;164-172/Region: protein kinase ATP-binding motif

Query Match 42.5%; Score 124.5; DB 2; Length 888; Best Local Similarity 50.9%; Pred. No. 6.9e-05; Indels 9; Gaps 3; Matches 28; Conservative 11; Mismatches 9;

Query Match 41.5%; Score 121.5; DB 2; Length 111; Best Local Similarity 49.1%; Pred. No. 1.8e-05; Indels 9; Gaps 3; Matches 27; Conservative 10; Mismatches 9;

RESULT 7
 Query 1 HRDIKAGNINILLEKEHDDICNKTLKITDFGLAREW-HRTIKSTACTYAWAPE 54
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: JC3399
 C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 28-May-1999
 R;Matsut, N.; Sarkar, G.; Shuto, T.; Mars, J.; Bronk, J.T.; Mizuno, K.; Belander, M.E. Biochem. Biophys. Res. Commun. 229, 571-576, 1996
 A;Title: Identification of a dual leucine zipper kinase involved in rat fracture repair.
 A;Reference number: JC3399; MUID:97127443; PMID:8954939
 A;Accession: JC3399
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-888 <MAY>
 C;Comments: This enzyme is involved in regulating cell function in the musculoskeletal system
 C;Genetics: IDK
 A;Gene: IDK
 C;Keywords: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs; protein kinase ATP-binding motif F;54-89/Region: leucine zipper motif F;156-454/Region: kinase catalytic #status predicted <CAT> F;156-404/Region: protein kinase homology <KIN> F;164-172/Region: protein kinase ATP-binding motif F;422-449/Region: leucine zipper motif F;472-500/Region: leucine zipper motif F;557-888/Region: glycine-serine-proline rich #status predicted

Query Match 41.3%; Score 121; DB 2; Length 356; Best Local Similarity 51.8%; Pred. No. 6.3e-05; Indels 10; Gaps 4; Matches 29; Conservative 7; Mismatches 10;

Query Match 41.3%; Score 121; DB 2; Length 356; Best Local Similarity 51.8%; Pred. No. 6.3e-05; Indels 10; Gaps 4; Matches 29; Conservative 7; Mismatches 10;

RESULT 8
 Query 1 HRDIKAGNINILLEKEHDDICNKTLKITDFGLAREW-HRTIKSTACTYAWAPE 54
 C;Species: Homo sapiens (man)
 C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 24-Sep-1999
 C;Accession: I38218; S7420
 R;Schultz, S.J.; Niqg, E.A. Cell Growth Differ. 4, 821-830, 1993
 A;Title: Identification of 21 novel human protein kinases, including 3 members of a family.
 A;Reference number: I38211; MUID:94100173; PMID:8274451
 A;Accession: I38218
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-111 <RTE>
 A;Cross-references: EMBL:Z225428; NID:9405734; PIDN:CAA80915; PID:9405735
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homologs; protein kinase homology <KIN>
 C;Keywords: ATP; leucine zipper; phosphotransferase F;1-111/Region: protein kinase homology (fragment)

Query Match 41.5%; Score 121.5; DB 2; Length 111; Best Local Similarity 49.1%; Pred. No. 1.8e-05; Indels 9; Gaps 3; Matches 27; Conservative 10; Mismatches 9;

Query Match 41.5%; Score 121.5; DB 2; Length 111; Best Local Similarity 49.1%; Pred. No. 1.8e-05; Indels 9; Gaps 3; Matches 27; Conservative 10; Mismatches 9;

RESULT 9
 Query 1 HRDIKAGNINILLEKEHDDICNKTLKITDFGLAREW-HRTIKSTACTYAWAPE 54
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 15-Feb-1995 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C;Accession: S61766
 R;Irregar, J.; Jouanic, S.; Schwobel-Dugue, N.; Kreis, M. submitted to the EMBL Data Library, November 1995
 A;Description: An unusual protein kinase displaying characteristics of both the serin and threonine protein kinase ATNL (EC 2.7.1.-) - Arabidopsis thaliana
 A;Reference number: S61766
 A;Accession: S61766
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X92728; NID:91054632; PIDN:CAA63387; PID:91054633
 C;Genetics:
 A;Gene: ATNL
 C;Keywords: kinase-related transforming protein; protein kinase homology F;24-233/Region: protein kinase homology <KIN>
 F;32-40/Region: protein kinase ATP-binding motif

Query Match 41.3%; Score 121; DB 2; Length 356; Best Local Similarity 51.8%; Pred. No. 6.3e-05; Indels 10; Gaps 4; Matches 29; Conservative 7; Mismatches 10;

Query Match 41.3%; Score 121; DB 2; Length 356; Best Local Similarity 51.8%; Pred. No. 6.3e-05; Indels 10; Gaps 4; Matches 29; Conservative 7; Mismatches 10;

RESULT 10
 Query 1 HRDIKAGNINILLEKEHDDICNKTLKITDFGLAREW-HRTIKSTACTYAWAPE 54
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C;Accession: T05675
 R;Bevan, M.; Wedler, H.; Kutner, M.; Wanburt, R.; Bancroft, I.; Mewes, H.W.; Mayer, A;Reference number: Z15420
 A;Accession: T05675
 A;Molecule type: DNA
 A;Residues: 1-545 <REV>
 A;Cross-references: EMBL:AL035540
 A;Experimental source: cultivar Columbia; BAC clone F20M13
 C;Genetics:

A: Map position: 4 108/3; 164/2; 204/2; 222/3; 259/3; 276/3; 328/2; 353/1; 411/3; 443/3; 4
A: Introns: 70/7; 108/3; 164/2; 204/2; 222/3; 259/3; 276/3; 328/2; 353/1; 411/3; 443/3; 4
A: Note: F20M13..30

Query Match 39.1%; Score 114.5; DB 2; Length 545;
Best Local Similarity 45.5%; Pred. No. 0.00042; Conway, A.B.; Kaul, S.; White, O.; Alon
Matches 25; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

Qy 1 HRDIKAGNTILLEKIEHDICNKLTKITDREGAREWHRHRTKMSI-AGYAWAPE 54
Db 397 HRDLKAANLIMDE-----NEVVKVADFUVARVKAQIGVMTAETGTYRWHAPE 443

RESULT 11

A: Reference number: 22447; MUID: 9919696; PMID: 10095117

A: Accession: T26266

C: Species: Arabidopsis thaliana (mouse-ear cress)

C: Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 08-Dec-2000

C: Accession: T26266

R: Jouannic, S.; Hamal, A.; Leprince, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.

A: Title: Characterisation of novel plant genes encoding MEKK/STE11 and RAF-related proteins

A: Reference number: 22447; MUID: 9919696; PMID: 10095117

A: Status: Preliminary; translated from GB/EMBL/DBDJ

A: Molecule type: mRNA

A: Residues: 1-406 <CDS>

A: Cross-references: EMBL:Y14199; NID:92253009; PIDN:CAA74591.1; PID:92253010

A: Experimental source: cultivar Columbia

C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 37.9%; Score 111; DB 2; Length 406;
Best Local Similarity 48.2%; Pred. No. 0.00071; Mismatches 11; Indels 10; Gaps 3;
Matches 27; Conservative 8;

Qy 1 HRDIKAGNTILLEKIEHDICNKLTKITDREGAREWHRHRT--TRNSTAGTYAWEPE 54
Db 256 HRDLKSPN-LLVDR-----NWVVKVCDRGLSLRKHHTYLSSKSTAGTPENMAPE 303

RESULT 12

A: Reference number: 224490

A: Accession: T28544

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-886 <BEV>

A: Cross-references: EMBL:AL163812

A: Experimental source: cultivar Columbia; BAC clone F14F18

C: Genetics:

A: Map position: 5 148/3; 180/3; 327/3; 362/2; 568/3; 658/1; 671/3; 694/3; 728/2; 754/3; 810/3;
A: Introns: 148/3; 180/3; 327/3; 362/2; 568/3; 658/1; 671/3; 694/3; 728/2; 754/3; 810/3;
A: Note: F14F18..20

Query Match 37.9%; Score 111; DB 2; Length 886;
Best Local Similarity 48.2%; Pred. No. 0.0015; Mismatches 11; Indels 10; Gaps 3;
Matches 27; Conservative 8;

Qy 1 HRDIKAGNTILLEKIEHDICNKLTKITDREGAREWHRHRT--TRNSTAGTYAWEPE 54
Db 770 HRDLKSPN-LLVDR-----NWVVKVCDRGLSLRKHHTYLSSKSTAGTPENMAPE 817

RESULT 13

F9673 hypothetical protein_F25P22.8 [imported] - Arabidopsis thaliana

A: Residues: 1-58, '1', 50-263, 'P', 265-278, 'I', 280-702, 'S', 707-708, 'RP', 714, 'VITME', 715

C: Species: Arabidopsis thaliana (mouse-ear cress)

C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C: Accession: F9673

R: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar,
Aisen, N.F.; Hughes, B.; Huijzer, L.; Nature 408; 816-820; 2000

A: Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Mazia,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Taliol
A: Authors: Salzberg, S.L.; Schwartz, J.R.; Venter, J.C.; Davis, R.W.
A: Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A: Reference number: A86141; MUID: 21016719; PMID: 1130712

A: Accession: F9673

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-1030 <STO>

A: Cross-references: GB:AE005173; NID:96692730; PIDN:AAF24836.1; GSPDB:GN00141

C: Genetics:

A: Gene: F25P22.8

A: Map Position: 1

Query Match 37.9%; Score 111; DB 2; Length 1030;
Best Local Similarity 48.2%; Pred. No. 0.0018; Mismatches 11; Indels 10; Gaps 3;
Matches 27; Conservative 8;

Qy 1 HRDIKAGNTILLEKIEHDICNKLTKITDREGAREWHRHRT--TRNSTAGTYAWEPE 54
Db 869 HRDLKSPN-LLVDR-----NWVVKVCDRGLSLRKHHTYLSSKSTAGTPENMAPE 916

RESULT 14

S20117

A: Reference number: S20117

A: Accession: S20117

A: Status: Preliminary

A: Molecule type: DNA

A: Residues: 1-1478 <COS>

A: Cross-references: EMBL:MB4389

A: Experimental source: strain S288C

R: Miosca, T.; Boles, E.; Schaaf-Gerstenschaeger, I.; Schmitt, S.; Zimmermann, F.K.
Yeast 10, 1481-1488; 1994

A: Title: Sequence and function analysis of a 9.74 kb fragment of *Saccharomyces cerevisiae*

A: Reference number: S50295; MUID: 95176706; PMID: 7871887

A: Accession: S50298

A: Status: nucleic acid sequence not shown

A: Molecule type: DNA

A: Residues: 1-1478 <DNA>

A: Cross-references: EMBL:X77923; NID:9640004; PIDN:CAA54896.1; PMID: 9640009

R: Lee, K.S.; Levin, D.E.
Mol. Biol. 12: 172-182; 1992

A: Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass

A: Reference number: S22285

A: Accession: S22285

A: Molecule type: DNA

A: Residues: 1-88, '1', 60-1478 <BEV>

R: Lee, K.S.; Levin, D.E.
Mol. Biol. 12: 172-182; 1992

A: Experimental source: strain EG123

R: Lee, K.S.; Levin, D.E.
submitted to the EMBL Data Library, June 1991

A: Description: An extragenic suppressor of mutations in the *S. cerevisiae* protein kinase

A: Reference number: S19061

A: Accession: S19061

A: Molecule type: DNA

A: Residues: 1-58, '1', 50-263, 'P', 265-278, 'I', 280-702, 'S', 707-708, 'RP', 714, 'VITME', 715

A;Cross-references: EMBL:X60227; NID:93414; PIDN:CAA42788.1; PID:93415
 A;Experimental source: strain EG123
 R;Irie, K.; Arai, H.; Oshima, Y.
 Gene 108, 139-144, 1991
 A;Title: A new protein kinase, SSP31, modulating the SMP3 gene-product involved in plasm

A;Reference number: JQ1432; MUID:92104496; PMID:1840547
 A;Accession: JQ1432

A;Molecule type: DNA

A;Residues: 149-1478 <TRT>

A;Cross-references: EMBL:D10389; DDBJ:D90445
 R;Mosga, T.; Schaafft-Geistenschaefer, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournie

submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56855
 A;Accession: SS56872

A;Molecule type: DNA

A;Residues: 1-1478 <MW>

A;Cross-references: EMBL:Z49370; NID:91008269; PIDN:CAA89389.1; PID:91008270; MIPS:YJL09

R;Cusick, M.E.
 submitted to the EMBL Data Library, March 1992

A;Reference number: S27437

A;Accession: S30794

A;Molecule type: DNA

A;Residues: 602-959, 'R', '961, 'R', '963-1085, 'V', 1087, 'SLLIAHT', 1092-1094, 'RMD', 1101, 'TV', 11

A;Cross-references: EMBL:N88604; NID:9172073; PIDN:AA21179.1; PID:9172074

A;Gene: SGD:BCK1; SLK1; SSP31

A;Cross-references: SGD:S0003631; MIPS:YJL095w

A;Map position: 10L

C;Function:

A;Description: phosphotransferase; protein kinase; involved in cell proliferation

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C;Keywords: ATP; Phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F:1173-1440|Domain: protein kinase homology <KIN>

F:1181-1189|Region: protein kinase ATP-binding motif

C;Function:

Query Match 37.0%; Score 108.5; DB 2; Length 1478;

Best Local Similarity 43.9%; Pred. No. 0.0044; Matches: 10; Mismatches: 11; Indels 11; Gaps 3;

Matches 25; Conservative 10; Mismatches: 11; Indels 11; Gaps 3;

QY 1 HRDIKAGNLLEKIEHDICNKVILKTDGFLAREWHRKTMS-TAGTYAWMAPE 54

Db 1301 HRDKADNLLE---DODGIC---KISDFEISKRSKDIISNSDMMRGYFWMAPE 1349

RESULT 15

G8635 probable protein kinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002

C;Accession: G84635
 C;Gene: At2g3360

M;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M;Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Newman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84635

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-407 <STO>

A;Cross-references: GB:AE002093; NID:94337195; PIDN:AD18109.1; GSDB:GN00139

C;Genetics:
 C;Map position: 2

C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 36.7%; Score 107.5; DB 2; Length 407;
 Best Local Similarity 43.6%; Pred. No. 0.0016; Matches 10; Mismatches 12; Indels 9; Gaps 2;

Matches 24; Conservative 10; Mismatches 12; Indels 9; Gaps 2;

QY 1 HRDIKAGNLLEKIEHDICNKVILKTDGFLAREWHRKTMS-TAGTYAWMAPE 54

Db 250 HRDIKSDNLLE-----SADKSIIKADFGVARIEVOTEGMPETGTYWRMAPE 296

Search completed: December 13, 2002, 23:32:06
 Job time : 48 secs

